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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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EXAMINER	
STEADMAN, DAVID J	

ART UNIT	PAPER NUMBER
1656	

DATE MAILED: 03/17/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/955,737	CHOPRA ET AL.	
	Examiner	Art Unit	
	David J. Steadman	1656	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *28 April 2005 and 31 May 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *9-27 and 31-34* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *9-27 and 31-34* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *31 May 2005* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *4/28/05*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Status of the Application

[1] The Art Unit location of your application in the USPTO has changed. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to Art Unit 1656.

[2] Claims 9-27 and 31-34 are pending in the application.

[3] Applicant's amendment to the claims, filed on 4/28/2005, is acknowledged. This listing of the claims replaces all prior versions and listings of the claims.

[4] Applicant's amendment to the specification, filed on 4/28/2005, is acknowledged.

[5] Applicant's amendments to the drawing figures, filed on 4/28/2005 and 5/31/2005, are acknowledged. The amendment filed on 4/28/2005 fails to comply with 37 CFR § 1.121 for reasons set forth in the Office communication mailed on 5/9/2005. The amendment filed on 5/31/2005 appears to correct the noted deficiency.

[6] Applicant's arguments filed on 4/28/2005 are acknowledged. Applicant's arguments have been fully considered and are deemed to be persuasive to overcome some of the rejections and/or objections previously applied. Rejections and/or objections not reiterated from previous office actions are hereby withdrawn.

[7] The text of those sections of Title 35 U.S. Code not included in the instant action can be found in a prior Office action.

Information Disclosure Statement

[8] All references cited in the information disclosure statement (IDS) filed on 4/28/2005 have been considered by the examiner. A copy of Form PTO-1449 is attached to the instant Office action.

Claim Rejections - 35 USC § 112, First Paragraph

[9] The written description rejection of claims 9-27 under 35 U.S.C. 112, first paragraph, is maintained for the reasons of record and the reasons stated below. The rejection was fully explained in the prior Office action. Newly added claims 31-34 are included in the rejection. Thus, claims 9-27 and 31-34 are rejected.

RESPONSE TO ARGUMENT: Applicant argues: 1) the claims are limited by the polypeptides covered by the claims and the coordinates thereof and 2) the specification defines "active site" and provides relevant identifying characteristics of the recited active site.

Applicants' argument is not found persuasive. The examiner maintains the position that the single disclosed species of 3-D models of BACE, *i.e.,* the 3-D structure of BACE having the structural coordinates of Figure 1, and active site residues thereof as disclosed at p. 9, ¶¶[0031] to [0032] of the specification, fails to reflect the variation among the members of the recited genus of 3-D models of BACE or APP binding proteins generated using the "relative structural coordinates" as "represented in" Figure 1 or specific amino acids positions thereof, having a rmsd from the backbone atoms of not more than 1.5, 1.0, or 0.5 Å and active sites thereof. As noted in the prior Office action, the genus of 3-D models of BACE or APP binding proteins encompasses

species that are *widely* variant. It is noted that the genus of 3-D models of BACE or APP binding proteins are generated *using* the *"relative structural coordinates"* as *"represented in"* Figure 1 or specific amino acids positions thereof. Because the 3-D model is generated "using" structural coordinates, the claims have been interpreted in accordance with MPEP 2111 as including any homology model of BACE or an APP binding protein having any structure. It is further noted that the claims recite "relative structural coordinates." At p. 6, ¶[0021], the specification states "...it is recognized that the structural coordinates of the present invention are relative, and are in no way specifically limited by the actual x, y, z coordinates of FIG. 1." Thus, according to the specification, "relative structural coordinates" are not limited to those disclosed in Figure 1, but can be any structural coordinates. Also, it is noted that, in view of the recitation of "represented in" with respect to the structural coordinates of Figure 1, the claims have been broadly interpreted according to MPEP 2111 as encompassing any representation of the structural coordinates of Figure 1, including homology models having any structure. In this case, the specification discloses only a single species of the genus of 3-D models of BACE or an APP binding protein, *i.e.,* the 3-D model of BACE having the structural coordinates of Figure 1. Other than this single species, the specification fails to disclose any other representative species. As noted in the prior Office action, when there is substantial variation within the genus, MPEP § 2163 states one must describe a sufficient variety of species to reflect the variation within the genus. While MPEP § 2163 acknowledges that in certain situations "one species adequately supports a genus," it is also acknowledges that "[f]or inventions in an unpredictable art, adequate written

description of a genus which embraces widely variant species cannot be achieved by disclosing only one species within the genus." In this case, the single disclosed species fails to reflect the substantial variation among members of the genus.

It is also noted that the genus of active site residues of claim 9 is unlimited. The specification discloses that "'active site' refers to a region of a molecule or molecular complex that, as a result of its shape and charge potential, favorably interacts or associates with another agent (including, without limitation, a protein, polypeptide, peptide, nucleic acid, including DNA or RNA, molecule, compound, antibiotic or drug) via various covalent and/or non-covalent binding forces," which is meant to include the "actual site in which BACE binds and cleaves APP, as well as accessory binding sites adjacent or proximal to the actual binding site that nonetheless may affect the ability of BACE to bind and cleave APP" and "BACE analog residues which exhibit observable NMR perturbations in the presence of a binding ligand" (specification at pp. 7-8, ¶¶[0026] and [0027]). Thus, the genus of active sites is not limited to those residues disclosed in the specification at p. 9, ¶¶[0031] to [0032], but to any region of any 3-D structure as noted above that "favorably interacts or associates with another agent." The disclosed active site of BACE fails to reflect the variation among the species of active sites as encompassed by the claims.

It is also noted that claims 16, 19, 24, and 27 involve steps of contacting the agent with BACE or an APP binding protein optionally in the presence of APP and optionally to determine the effect of the agent on BACE or the APP binding protein. The examiner has interpreted the claims as meaning the contacting step is a *physical*, *i.e.*,

ex silico, contacting of a BACE or APP binding protein with the agent obtained in the last step of claim 12 or 20. The specification discloses only a single species of BACE polypeptides or APP binding proteins, *i.e.,* SEQ ID NO:1, and discloses only a single species of APP proteins, *i.e.,* SEQ ID NO:2. Other than this single species of the genus of BACE or APP polypeptides, the specification fails to disclose any other representative species, which encompasses widely variant species of polypeptides. As noted above, MPEP § 2163 states that "[f]or inventions in an unpredictable art, adequate written description of a genus which embraces widely variant species cannot be achieved by disclosing only one species within the genus."

Given the lack of description of a representative number of candidate modulators or potential inhibitors, the specification fails to sufficiently describe the claimed invention in such full, clear, concise, and exact terms that a skilled artisan would recognize that applicant was in possession of the claimed invention.

[10] The scope of enablement rejection of claims 9-27 under 35 U.S.C. 112, first paragraph, is maintained for the reasons of record and the reasons stated below. The rejection was fully explained in the prior Office action. Newly added claims 31-34 are included in the rejection. Thus, claims 9-27 and 31-34 are rejected.

RESPONSE TO ARGUMENT: Regarding the breadth of the claims, applicant argues the scope of the claims is no broader than applicant's contribution.

Applicants' argument is not found persuasive. The specification discloses only a single working example of a 3-D model of BACE, *i.e.,* the 3-D model of BACE having

the structural coordinates of Figure 1 and only a single active site thereof, *i.e.,* those amino acids as disclosed at p. 9, ¶¶[0031] to [0032] of the specification. However, the claims are so broad as to encompass the use of all 3-D models of BACE or APP binding proteins that are generated *using* the *"relative structural coordinates"* as *"represented in"* Figure 1 or specific amino acids positions thereof. Because the 3-D model is generated "using" structural coordinates, the claims have been interpreted in accordance with MPEP 2111 as including any homology model of BACE or an APP binding protein having any structure. It is further noted that the claims recite "relative structural coordinates." At p. 6, ¶[0021], the specification states "...it is recognized that the structural coordinates of the present invention are relative, and are in no way specifically limited by the actual x, y, z coordinates of FIG. 1." Thus, according to the specification, "relative structural coordinates" are not limited to those disclosed in Figure 1, but can be any structural coordinates. Also, it is noted that, in view of the recitation of "represented in" with respect to the structural coordinates of Figure 1, the claims have been broadly interpreted according to MPEP 2111 as encompassing any representation of the structural coordinates of Figure 1, including homology models having any structure. Also, regarding the scope of active sites, the specification discloses that "'active site' refers to a region of a molecule or molecular complex that, as a result of its shape and charge potential, favorably interacts or associates with another agent (including, without limitation, a protein, polypeptide, peptide, nucleic acid, including DNA or RNA, molecule, compound, antibiotic or drug) via various covalent and/or non-covalent binding forces," which is meant to include the "actual site in which BACE binds

and cleaves APP, as well as accessory binding sites adjacent or proximal to the actual binding site that nonetheless may affect the ability of BACE to bind and cleave APP" and "BACE analog residues which exhibit observable NMR perturbations in the presence of a binding ligand" (specification at pp. 7-8, ¶¶[0026] and [0027]). Thus, the active site is not limited to those residues disclosed in the specification at p. 9, ¶¶[0031] to [0032], but to *any* region of any 3-D structure as noted above that "favorably interacts or associates with another agent." Further, it is noted that claims 16, 19, 24, and 27 involve steps of contacting the agent with BACE or an APP binding protein optionally in the presence of APP and optionally to determine the effect of the agent on BACE or the APP binding protein. The examiner has interpreted the claims as meaning the contacting step is a *physical, i.e., ex silico,* contacting of a BACE or APP binding protein with the agent obtained in the last step of claim 12 or 20. The claims encompass the use of *any* BACE, APP binding protein, or APP polypeptide having any sequence of amino acids.

Applicant summarizes the nature of the invention. The examiner agrees with applicant's characterization of the nature of the invention.

Applicant argues no one has previously disclosed or suggested the claimed methods. However, contrary to applicant's argument, the prior art taught or suggested the claimed methods.

Applicant asserts a skilled artisan in this field of endeavor would likely have an advanced degree. The examiner agrees with applicant's assertion.

Applicant argues that while the relevant art is generally unpredictable, the application provides sufficient guidance to allow a skilled artisan to practice the full scope of the claimed invention.

Applicants' argument is not found persuasive. At the time of the invention, methods for displaying a 3-D structure of a polypeptide and generating homology models were known in the prior art. However, while methods of generating homology models of a protein using a set of structure coordinates was known, Lambert et al. (US Patent Application Publication 2004/0137518) acknowledges that "[p]otential or existent homology models cannot provide the necessary degree of specificity" in the *in silico* design of modulators (p. 3, ¶[0017]). Further, it was well-known in the prior art that polypeptides having disparate functions can share similar 3-D structures. For example, Hegyi et al. [*J Mol Biol* (1999) 288:147-164; cited in the prior Office action] teaches that an isomerase, an oxidoreductase, a hydrolase, and a lyase all share the same TIM-barrel fold (p. 148, left column, and Figure 1). Thus, a skilled artisan would have recognized that there was a high level of unpredictability in using altered 3-D protein structures as encompassed by the claims with an expectation that the altered 3-D structures represent a biologically relevant conformation of BACE.

Furthermore, as noted above, the claims encompass the use of any BACE, APP binding protein, or APP polypeptide, including mutants and variants, and it is highly unpredictable as to the effects of altering the amino acid sequence of a polypeptide and the resulting effects on the activity of the mutant or variant polypeptide.

Applicant argues the specification discloses a working example and additional guidance regarding active sites and agents that interact therewith.

In this case, the specification discloses only a single working example of a 3-D structure of BACE or an APP binding protein, *i.e.,* the 3-D structure of BACE having the structural coordinates of Figure 1 and only a single working example of an active site thereof, *i.e.,* those residues disclosed in the specification at p. 9, ¶¶[0031] to [0032]. The specification fails to provide guidance for making and using any other 3-D structure as broadly encompassed by the claims for identifying an interacting agent with an expectation that the identified agent would have the ability to bind BACE *in vitro* or *in vivo*. Further, the specification discloses only a single working example of BACE polypeptides or APP binding proteins, *i.e.,* SEQ ID NO:1, and discloses only a single working example of APP proteins, *i.e.,* SEQ ID NO:2.

Applicant argues that in view of the disclosure, undue experimentation is not required to practice the full scope of the claimed invention.

Applicants' argument is not found persuasive. While methods of altering a 3-D structure of a protein *in silico* and methods of mutating a polypeptide's sequence were known at the time of the invention, it was not routine in the art to create a substantial number of altered 3-D structures or polypeptides as encompassed by the claims without guidance as to which of those is useful in accordance with the asserted utility of the claimed invention, *i.e.,* "in rational drug design methods to identify agents that may interact with active sites of BACE" that "may represent new therapeutics" (specification at p. 1, ¶ [0002]).

Thus, in view of the lack of guidance and working examples provided in the specification, the high level of unpredictability, and the significant amount of experimentation required, undue experimentation would be necessary for a skilled artisan to make and use the claimed invention.

Claim Rejections - 35 USC § 102

[11] The rejection of claims 9-27 under 35 U.S.C. 102(e) as anticipated by or, in the alternative, under 35 U.S.C. 103(a) as obvious over Tang et al. is maintained for the reasons of record and the reasons stated below. Claims 31-34 have been included in the instant rejection. Thus, claims 9-27 and 31-34 are rejected.

RESPONSE TO ARGUMENT: Applicant argues Tang et al. does not disclose the structural coordinates of Figure 1 because the residues of BACE in the crystal of Tang et al. are amino acids 14 to 454, while the residues of BACE of the instantly disclosed crystal are amino acids 47 to 460 plus 9 amino acids due to a cloning artifact.

Applicant's argument is not found persuasive. As noted above, there is no requirement in the claims that the 3-D structure of BACE or APP binding protein be limited to having the structural coordinates of Figure 1. Although the claims are interpreted in light of the specification, limitations from the specification are not read into the claims. See *In re Van Geuns*, 988 F.2d 1181, 26 USPQ2d 1057 (Fed. Cir. 1993).

Instead, the claims encompass the use of 3-D models of BACE or APP binding proteins that are generated *using* the *"relative structural coordinates"* as *"represented in"* Figure 1 or specific amino acids positions thereof. Because the 3-D model is

generated "using" structural coordinates, the claims have been interpreted in accordance with MPEP 2111 as including any homology model of BACE or an APP binding protein having any structure. It is further noted that the claims recite "relative structural coordinates." At p. 6, ¶[0021], the specification states "...it is recognized that the structural coordinates of the present invention are relative, and are in no way specifically limited by the actual x, y, z coordinates of FIG. 1." Thus, according to the specification, "relative structural coordinates" are not limited to those disclosed in Figure 1, but can be any structural coordinates. Also, it is noted that, in view of the recitation of "represented in" with respect to the structural coordinates of Figure 1, the claims have been broadly interpreted according to MPEP 2111 as encompassing any representation of the structural coordinates of Figure 1, including homology models having any structure. Thus, in view of the broad but reasonable interpretation of the claims in accordance with MPEP 2111, the 3-D models of Tang et al. (*e.g.,* the models shown in Figures 6-7 and 9) fall within the scope of recited 3-D models as recited in the claims. Consequently, the teachings of Tang et al. anticipates the claimed methods.

Claim Rejections - 35 USC § 103

[12] Claim(s) 9-19, 21, and 31-33 are rejected under 35 U.S.C. 103(a) as being unpatentable over Sauder et al. in view of Anderson et al. (US Patent 5,942,400). The claims are drawn to methods for identifying an agent that interacts with an active site of BACE or an APP binding protein or peptide.

The reference of Sauder et al. teaches a method of computer modeling of human BACE with APP and APP mutant substrates to determine the substrate specificity of BACE (see pp. 244-246, particularly Figure 4). Sauder et al. discloses amino acids that are involved in the interaction of BACE and APP and APP mutant substrates (p. 246). Sauder et al. teaches "[i]nhibitors that bind to the BACE active site may prove useful for drugs to treat and prevent Alzheimer's disease" (abstract). The reference of Sauder et al. does not teach obtaining APP or APP mutant substrates or screening APP or mutants thereof for their effect on BACE or APP binding protein.

Anderson et al. teaches methods for producing purified human BACE (columns 27-28; referred to as beta-secretase by Anderson et al.) and using the purified BACE in an *in vitro* screening assay to identify BACE inhibitors (columns 28-30). Anderson et al. teaches a BACE inhibitor identified by the screening assay (Figure 18).

At the time of the invention, it would have been obvious to one of ordinary skill in the art to model the inhibitor of Anderson et al. with BACE according to Sauder et al., synthesize the agent, and screen the agent for its ability to inhibit BACE activity. One would have been motivated to model the inhibitor of Anderson et al. with BACE according to Sauder et al. in order to determine the substrate specificity of the inhibitor, synthesize the agent, and screen the agent for its ability to inhibit BACE activity. One would have a reasonable expectation of success for to modeling the inhibitor of Anderson et al. with BACE according to Sauder et al., synthesizing the agent, and screening the agent for its ability to inhibit BACE activity because of the results of Sauder et al. and Anderson et al. Therefore, claims 9-19, 21, and 31-33, drawn to

methods for identifying an agent that interacts with an active site of BACE or an APP binding protein or peptide as described above would have been obvious to one of ordinary skill in the art at the time of the invention.

RESPONSE TO ARGUMENT: Applicant argues the reference of Sauder et al. does not disclose the "relative structural coordinates" of Figure 1 because the structural coordinates of Sauder et al. have gaps at residues 220-229, 319-325, and 345-355. Applicant argues these gaps do not exist in the structural coordinates of Figure 1 and thus Sauder et al. does not anticipate the claimed invention.

Applicants' argument is not found persuasive. The residues identified by applicant as not being included in the structural coordinates of Sauder et al., *i.e.,* residues 220-229, 319-325, and 345-355, are not required in the claims. Although the claims are interpreted in light of the specification, limitations from the specification are not read into the claims. See *In re Van Geuns*, 988 F.2d 1181, 26 USPQ2d 1057 (Fed. Cir. 1993).

[13] The rejection of claim(s) 9-15, 17-18, 20-23, and 25-26 under 35 U.S.C. 103(a) as being unpatentable over Balaji et al. (US Patent 5,579,250) in view *In re Gulack* 217 USPQ 401 (Fed. Cir. 1983) is maintained for the reasons of record and the reasons stated below. Newly added claims 31-34 are included in the instant rejection. Thus, claims 9-15, 17-18, 20-23, 25-26, and 31-34 are rejected.

RESPONSE TO ARGUMENT: Applicant argues the claims require obtaining an agent, which according to applicant, the cited references fail to teach or suggest.

Applicant's argument is not found persuasive. The reference of Balaji et al. clearly teaches obtaining the compound by synthesizing the desired compound identified by the disclosed method of rational drug design (see particularly columns 27-31).

[14] Claim(s) 16, 19, 24, and 27 are rejected under 35 U.S.C. 103(a) as being unpatentable over Balaji et al. in view *In re Gulack* 217 USPQ 401 (Fed. Cir. 1983) as applied to claims 9-15, 17-18, 20-23, 25-26, and 31-34 and further in view of Anderson et al. Claims 16, 19, 24, and 27 further limit claims 12, 18, 20, and 26 respectively, to contacting the agent with APP binding protein or BACE and optionally determining the effect of the agent on APP binding protein or BACE.

The teachings of Balaji et al. and *In re Gulack* are described above. The combination fails to teach contacting the agent with BACE or an APP binding protein optionally in the presence of APP to optionally determine the effect of the agent on BACE or the APP binding protein.

As noted above, Anderson et al. teaches methods for producing purified human BACE (columns 27-28; referred to as beta-secretase by Anderson et al.) and using the purified BACE in an *in vitro* screening assay along with APP or fragments thereof to identify BACE inhibitors (columns 28-30).

Therefore, it would have been obvious to one of ordinary skill in the art at the time of the invention to perform rational drug design as taught by Balaji to result in an agent that interacts with BACE, wherein only nonfunctional descriptive material is additionally present in the claims, which do not distinguish the claimed methods from Balaji according to *In re Gulack* and to contact the resulting agent with BACE in order to determine whether the agent is a BACE inhibitor in accordance with Anderson et al. One would have been motivated to contact the agent identified by the method of Balaji et al. with BACE because of the teachings of Anderson et al. One would have had a reasonable expectation of success for contacting the agent identified by the method of Balaji et al. with BACE because of the teachings of Balaji et al. and Anderson et al. Therefore it would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains to employ the method of Balaji et al. using any set of structural coordinates as defined in the claims and contacting BACE with an identified agent as disclosed by Anderson et al.

Conclusion

[15] Status of the claims:

Claims 9-27 and 31-34 are pending.

Claims 9-27 and 31-34 are rejected.

No claim is in condition for allowance.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to David J. Steadman whose telephone number is 571-272-0942. The examiner can normally be reached on Mon to Fri, 7:30 am to 4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Kathleen Kerr can be reached on 571-272-0931. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1656